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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/718,102

DATE: 01/24/2002

TIME: 19:08:19

Input Set : N:\Crf3\RULE60\09718102.raw

Output Set: N:\CRF3\01242002\I718102.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Roncarolo, Maria-Grazia

6 de Waal Malefyt, Rene

7 Bacchetta, Rosa

8 Groux, Herve M.

9 de Vries, Jan E.

11 (ii) TITLE OF INVENTION: USE OF INTERLEUKIN-10 TO PRODUCE A

12 POPULATION OF SUPPRESSOR CELLS

14 (iii) NUMBER OF SEQUENCES: 26

16 (iv) CORRESPONDENCE ADDRESS:

17 (A) ADDRESSEE: DNAX Research Institute

18 (B) STREET: 901 California Avenue

19 (C) CITY: Palo Alto

20 (D) STATE: California

21 (E) COUNTRY: USA

22 (F) ZIP: 94304-1104

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: Apple Macintosh

27 (C) OPERATING SYSTEM: Macintosh 7.5.5

28 (D) SOFTWARE: Microsoft Word 5.1a

30 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/09/718,102

C--> 32 (B) FILING DATE: 20-Nov-2000

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

36 (A) APPLICATION NUMBER: 08/643,810

37 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Ching, Edwin P.

41 (B) REGISTRATION NUMBER: 34,090

42 (C) REFERENCE/DOCKET NUMBER: DX0261K1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 415-852-9196

46 (B) TELEFAX: 415-496-1200

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 178 amino acids

53 (B) TYPE: amino acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: peptide

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62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64 Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
65 1 5 10 15
67 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
68 20 25 30
70 Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
71 35 40 45
73 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
74 50 55 60
76 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
77 65 70 75 80
79 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
80 85 90 95
82 Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
83 100 105 110
85 Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Arg Cys His Arg
86 115 120 125
88 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
89 130 135 140
91 Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
92 145 150 155 160
94 Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
95 165 170 175
97 Arg Asn
100 (2) INFORMATION FOR SEQ ID NO: 2:
102 (i) SEQUENCE CHARACTERISTICS:
103 (A) LENGTH: 170 amino acids
104 (B) TYPE: amino acid
105 (C) STRANDEDNESS: single
106 (D) TOPOLOGY: linear
108 (ii) MOLECULE TYPE: peptide
113 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
115 Met Glu Arg Arg Leu Val Val Thr Leu Gln Cys Leu Val Leu Leu Tyr
116 1 5 10 15
118 Leu Ala Pro Glu Cys Gly Gly Thr Asp Gln Cys Asp Asn Phe Pro Gln
119 20 25 30
121 Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg Val Lys Thr Phe Phe
122 35 40 45
124 Gln Thr Lys Asp Glu Val Asp Asn Leu Leu Leu Lys Glu Ser Leu Leu
125 50 55 60
127 Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
128 65 70 75 80
130 Gln Phe Tyr Leu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro
131 85 90 95
133 Glu Ala Lys Asp His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu
134 100 105 110
136 Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys
137 115 120 125
139 Ser Lys Ala Val Glu Gln Ile Lys Asn Ala Phe Asn Lys Leu Gln Glu

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```

140          130          135          140
142      Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
143          145          150          155          160
145      Ile Glu Ala Tyr Met Thr Ile Lys Ala Arg
146          165          170

```

148 (2) INFORMATION FOR SEQ ID NO: 3:

150 (i) SEQUENCE CHARACTERISTICS:

151 (A) LENGTH: 160 amino acids

152 (B) TYPE: amino acid

153 (C) STRANDEDNESS: single

154 (D) TOPOLOGY: linear

156 (ii) MOLECULE TYPE: peptide

161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

163      Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His Phe Pro
164      1          5          10          15
166      Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe Ser Arg
167          20          25          30
169      Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu Leu Leu
170          35          40          45
172      Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala
173          50          55          60
175      Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala
176          65          70          75          80
178      Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu Gly Glu
179          85          90          95
181      Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu
182          100          105          110
184      Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn Ala Phe
185          115          120          125
187      Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp
188          130          135          140
190      Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile Arg Asn
191          145          150          155          160

```

194 (2) INFORMATION FOR SEQ ID NO: 4:

196 (i) SEQUENCE CHARACTERISTICS:

197 (A) LENGTH: 147 amino acids

198 (B) TYPE: amino acid

199 (C) STRANDEDNESS: single

200 (D) TOPOLOGY: linear

202 (ii) MOLECULE TYPE: peptide

207 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

209      Thr Asp Gln Cys Asp Asn Phe Pro Gln Met Leu Arg Asp Leu Arg Asp
210      1          5          10          15
212      Ala Phe Ser Arg Val Lys Thr Phe Phe Gln Thr Lys Asp Glu Val Asp
213          20          25          30
215      Asn Leu Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu
216          35          40          45
218      Gly Cys Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val
219          50          55          60

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```

221      Met Pro Gln Ala Glu Asn Gln Asp Pro Glu Ala Lys Asp His Val Asn
222      65                                70                                75                                80
224      Ser Leu Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys
225                                85                                90                                95
227      His Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Ile
228      100                                105                                110
230      Lys Asn Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met
231      115                                120                                125
233      Ser Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Ile
234      130                                135                                140
236      Lys Ala Arg
237      145
239 (2) INFORMATION FOR SEQ ID NO: 5:
241      (i) SEQUENCE CHARACTERISTICS:
242          (A) LENGTH: 15 base pairs
243          (B) TYPE: nucleic acid
244          (C) STRANDEDNESS: single
245          (D) TOPOLOGY: linear
247      (ii) MOLECULE TYPE: cDNA
252      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
254 CTAAGGAGGT TTAAC 15
256 (2) INFORMATION FOR SEQ ID NO: 6:
258      (i) SEQUENCE CHARACTERISTICS:
259          (A) LENGTH: 10 base pairs
260          (B) TYPE: nucleic acid
261          (C) STRANDEDNESS: single
262          (D) TOPOLOGY: linear
264      (ii) MOLECULE TYPE: cDNA
269      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
271 ATGAGCTCAT 10
273 (2) INFORMATION FOR SEQ ID NO: 7:
275      (i) SEQUENCE CHARACTERISTICS:
276          (A) LENGTH: 60 base pairs
277          (B) TYPE: nucleic acid
278          (C) STRANDEDNESS: single
279          (D) TOPOLOGY: linear
281      (ii) MOLECULE TYPE: cDNA
286      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
288 AGCCGAGGCC AGGGCACCCA GTCTGAGAAC AGCTGCACCC ACTTCCCAGG TAACCGGTAC 60
291 (2) INFORMATION FOR SEQ ID NO: 8:
293      (i) SEQUENCE CHARACTERISTICS:
294          (A) LENGTH: 56 base pairs
295          (B) TYPE: nucleic acid
296          (C) STRANDEDNESS: single
297          (D) TOPOLOGY: linear
299      (ii) MOLECULE TYPE: cDNA
304      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
306 CGGTTACCTG GGAAGTGGGT GCAGCTGTTC TCAGACTGGG TGCCCTGGCC TGGGCT 56
308 (2) INFORMATION FOR SEQ ID NO: 9:

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310      (i) SEQUENCE CHARACTERISTICS:
311          (A) LENGTH: 62 base pairs
312          (B) TYPE: nucleic acid
313          (C) STRANDEDNESS: single
314          (D) TOPOLOGY: linear
316      (ii) MOLECULE TYPE: cDNA
321      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
323 GTAACCTGCC TAACATGCTT CGAGATCTCC GAGATGCCTT CAGCAGAGTG AAGACTTTCT      60
325 TT                                                                    62
327 (2) INFORMATION FOR SEQ ID NO: 10:
329      (i) SEQUENCE CHARACTERISTICS:
330          (A) LENGTH: 48 base pairs
331          (B) TYPE: nucleic acid
332          (C) STRANDEDNESS: single
333          (D) TOPOLOGY: linear
335      (ii) MOLECULE TYPE: cDNA
340      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
342 CTTCACTCTG CTGAAGGCAT CTCGAGATC TCGAAGCATG TTAGGCAG      48
344 (2) INFORMATION FOR SEQ ID NO: 11:
346      (i) SEQUENCE CHARACTERISTICS:
347          (A) LENGTH: 35 base pairs
348          (B) TYPE: nucleic acid
349          (C) STRANDEDNESS: single
350          (D) TOPOLOGY: linear
352      (ii) MOLECULE TYPE: cDNA
357      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
359 CAAATGAAGG ATCAGCTGGA CAACTTGTTT TTAAG      35
361 (2) INFORMATION FOR SEQ ID NO: 12:
363      (i) SEQUENCE CHARACTERISTICS:
364          (A) LENGTH: 44 base pairs
365          (B) TYPE: nucleic acid
366          (C) STRANDEDNESS: single
367          (D) TOPOLOGY: linear
369      (ii) MOLECULE TYPE: cDNA
374      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
376 CTTAAGAACA AGTTGTCCAG CTGATCCTTC ATTTGAAAGA AAGT      44
378 (2) INFORMATION FOR SEQ ID NO: 13:
380      (i) SEQUENCE CHARACTERISTICS:
381          (A) LENGTH: 69 base pairs
382          (B) TYPE: nucleic acid
383          (C) STRANDEDNESS: single
384          (D) TOPOLOGY: linear
386      (ii) MOLECULE TYPE: cDNA
391      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
393 GAGTCCTTGC TGGAGGACTT TAAGGGTTAC CTGGGTTGCC AAGCCTTGTC TGAGATGATC      60
395 CAGTTTTAT                                                                69
397 (2) INFORMATION FOR SEQ ID NO: 14:
399      (i) SEQUENCE CHARACTERISTICS:
400          (A) LENGTH: 73 base pairs

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VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]